CLAIMS

We claim at least the following:

1. A method of performing nanopore data analysis, comprising:

providing a sample including target polymers and non-target polymers and a nanopore device, wherein the target polymers and non-target polymers are selected from polynucleotides and polypeptides;

introducing the sample to the nanopore device;

generating nanopore data points corresponding to each target polymer and each non-target polymer traversing an aperture of the nanopore;

forming a distribution pattern of the nanopore data points; and

analyzing a distribution of polymer data points in the distribution pattern.

2. The method of claim 1, wherein the distribution pattern includes at least one data cluster, and wherein analyzing includes analyzing the distribution of target polynucleotide data points within the at least one data cluster.

3. The method of claim 2, further comprising:

comparing the distribution of the target polynucleotide data points between two data clusters to a phosphorylation state standard distribution.

4. The method of claim 3, further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

5. The method of claim 2, further comprising:

determining a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

6. The method of claim 1, further comprising:

comparing a density distribution of the target polynucleotide data points to a chemical integrity standard density distribution, wherein a change in the density distribution of target polynucleotide data points as compared to the chemical integrity standard density distribution indicates that the chemical integrity of the target polynucleotides in the sample is different than a chemical integrity for which the chemical integrity standard density distribution was prepared.

7. The method of claim 6, further comprising:

determining the density of target polynucleotide data points in a defined area; and

comparing the density of the target polynucleotide data points to a chemical integrity standard density distribution for the defined area.

8. The method of claim 6, further comprising:

determining the density of target polynucleotide data points in a defined area;

comparing the density of the target polynucleotide data points to a density of the target polynucleotide data points of at least two other samples including target polynucleotides and non-target polynucleotides; and

ranking the samples based on the density of the target polynucleotide data points.

9. The method of claim 6, further comprising:

determining a cluster score for the target polynucleotide data points in a defined area; and

comparing the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area.

10. The method of claim 2, further comprising:

analyzing the distribution of the non-target polynucleotide data points.

11. The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that non-target polynucleotides have a different length than the target polynucleotides.

12. The method of claim 10, wherein distribution of non-target polynucleotide data points outside of the at least one cluster indicates that the non-target polynucleotides have the same length as the target polynucleotide but the sequence of the non-target polynucleotide and target polynucleotide is not the same.

13. The method of claim 10, further comprising:

determining a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

14. The method of claim 1, wherein the failure of polymer data points to form at least one cluster indicates that the target polymers in the sample represent less than a calibration specified fraction of the total polymers in the sample.

15. A system for performing nanopore data analysis, comprising:

a nanopore system including a nanopore device and a nanopore data analysis system, the nanopore device having a structure having an aperture, the nanopore data analysis system operative to:

generate nanopore data points corresponding to each target polymer and each non-target polymer traversing the aperture of the nanopore structure;

form a distribution pattern of the data points; and

analyze a distribution of target polymer data points in the distribution pattern.

16. The system of claim 15, wherein the nanopore data analysis system is further operative to analyze the distribution of the non-target polynucleotide data points.

17. The system of claim 16, wherein the nanopore data analysis system is further operative to determine a ratio between the target polynucleotide data points and the non-target polynucleotide data points.

18. The system of claim 18, wherein the distribution pattern includes at least one data cluster and wherein the nanopore data analysis system is further operative to:

analyze of the distribution of target polynucleotide data points between the two data clusters;

comparing the distribution of the target polynucleotide data points between the two data clusters to a phosphorylation state standard distribution; and

determine a ratio of phosphorylated target polynucleotide to non-phosphorylated target polynucleotides.

19. The system of claim 15, wherein the nanopore data analysis system is further operative to:

determine a cluster score for the target polynucleotide data points in a defined area; and

compare the cluster score for the target polynucleotide data points to a cluster score for a chemical integrity standard density distribution for the defined area in a distribution of a target polynucleotide standard.

20. The system of claim 15, wherein the nanopore data analysis system is stored on a computer-readable medium.

22. The system of claim 15, further comprising:

means for analyzing the distribution of target polynucleotide data points in the distribution pattern